

## SEQUENCE LISTING

SEQ ID NO:1            p33ING2 polypeptide sequence

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1  MLGQQQQQLY SSAALLTGER SRLLTCTYVD YLECVELPH DMQRNVSVLR
51  ELDNKYQETL KEIDDVYEKY KKEDDLNQKK RLQQLLQRAL INSQELGDEK
101 IQIVTQMLEL VENRARQMEL HSQCFQDPAE SERASDKAKM DSSQPERSSR
151 RPRRQRTSES RDLCHMANGI EDCDDQPPKE KKSksAKKKK RSKAKQEREA
201 SPVEFAIDPN EPTYCLCNQV SYGEMIGCDN EQCPIEFHF SCVSLTYKPK
251 GKWYCPKCRG DNEKTMKST ETKTKDRRSR

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SEQ ID NO:2            p33ING2 Nucleic acid sequence

(GenBank Accession No. AF053537)

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1  gcggccgcgg cgggtgcatg tgcggctgct ggatgcggag gcggcggcga cggcgcgat
61  cggcaggatg ttagggcagc agcagcagca actgtactcg tcggctgcgc tcctgaccgg
121 ggagcggagc cggctgctca cctgctacgt gcaggactac cttgagtgcg tggagtgcgt
181 gccccacgac atgcagagga acgtgtctgt gctgcgagag ctggacaaca aatatcaaga
241 aacgttaaag gaaattgatg atgtctacga aaaatataag aaagaagatg atttaaacca
301 gaagaaacgt ctacagcagc ttctccagag agcactaatt aatagtcaag aattgggaga
361 tgaaaaaata cagattgtta cacaatgct cgaattggtg gaaaatcggg caagacaaat
421 ggagttacac tcacagtgtt tccaagatcc tgctgaaagt gaacgagcct cagataaagc
481 aaagatggat tccagccaac cagaaagatc ttcaagaaga ccccgaggc agcggaccag
541 tgaaagccgt gatttatgtc acatggcaaa tgggattgaa gactgtgatg atcagccacc
601 taaagaaaag aaatccaagt cagcaaagaa aaagaaacgc tccaaggcca agcaggaaaag
661 ggaagcttca cctgttgagt ttgcaataga tcctaataaa cctacatact gcttatgcaa
721 ccaagtgtct tatggggaga tgataggatg tgacaatgaa cagtgtccaa ttgaatgggt
781 tcacttttca tgtgtttcac ttacctataa accaaagggg aaatggtatt gcccaaagtg
841 caggggagat aatgagaaaa caatggacaa aagtactgaa aagacaaaaa aggatagaag
901 atcgaggtag taaaggccat ccacatttta aagggttatt tgtcttttat ataattcggt
961 tgctttcaga aaatgtttta gggtaaatgc ataagactat gcaataattt ttaatcatta
1021 gtattaatgg tgtattaaaa gttgtgttac tttgaaaaaa aaaaaaaaaa aaaaaaaaaa

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SEQ ID NO:3 Primer            MLGQQQQQ

SEQ ID NO:4 Primer            KKDRRSR

SEQ ID NO:5 peptide 7-26 of p33ING2 (KMP1)

QQLYSSAALLTGERSRLTTC

SEQ ID NO:6 missense amino acid or nucleic acid sequence – arg 153 to ser

1 MLGQQQQQLY SSAALLTGER SRLLTCTYVD YLECVESLPH DMQRNVSVLR  
51 ELDNKYQETL KEIDDVYEKY KKEDDLNQKK RLQQLLQRAL INSQELGDEK  
101 IQIVTQMLEL VENRARQMEL HSQCFQDPAE SERASDKAKM DSSQPERSSR  
151 RPSRQRTSES RDLCHMANGI EDCDDQPPKE KKSksAKKKK RSKAKQEREA  
201 SPVEFAIDPN EPTYCLCNQV SYGEMIGCDN EQCPIEFHF SCVSLTYKPK  
251 GKWYCPKCRG DNEKTMDKST ETKKDRRSR

SEQ ID NO:7 p33ING2 genomic DNA sequence (Exon1/Intron)  
(GenBank Accession No. HSING2S1)

Exon 1: 1..239

Intron: 240...>423

1 gcggccgcgg ccggtgcatg tgcggctgct ggatgcggag gcggcggcga cggcgcggtat  
61 cggcaggatg ttagggcagc agcagcagca actgtactcg tcggctgcgc tcctgaccgg  
121 ggagcggagc cggctgctca cctgctacgt gcaggactac cttgagtgcg tggagtgcgt  
181 gccccacgac atgcagagga acgtgtctgt gctgcgagag ctggacaaca aatatcaagg  
241 taggggcccgc ggggctgccg gcctcgggag ccggtggcgg ggagcctgtc cgggggagtg  
301 ccaccttccc tttctcccgt gacagtctcc ccgagcgcac cgaggggtctg ccgagcggga  
361 ctgggaggac tggagaccgg gttggcggcc ctccgtggcc ccgcggtggg cgagtgaagg  
421 aga

SEQ ID NO:8 p33ING1 amino acid sequence

p33ING1 Length: 279

1 MLSPANGEQL HLVNYVEDYL DSIESLPFDL QRNVSLMREI DAKYQEILKE  
51 LDECYERFSR ETDGAQKRRM LHCVRALIR SQELGDEKIQ IVSQMVOLVE  
101 NRTRQVDSHV ELFEAQQLG DTAGNSGKAG ADRPKGEAAA QADKPNKRS  
151 RRQRNNENRE NASSNHDHDD GASGTPKEKK AKTSKKKKRS KAKAEREASP  
201 ADLPIDPNP TYCLCNQVSY GEMIGCDNDE CPIEFHFHSC VGLNHKPKGK  
251 WYCPKCRGEN EKTMDKALEK SKKERAYNR

SEQ ID NO:9 Peptide 1-17 and C of p33ING1 (KMP2)

MLSPANGEQLHLVNYVEC

SEQ ID NO:10 p33ING2 genomic DNA sequence (Exon 2/intron)  
(GenBank Accession No. HSING2S2)

Intron: <1..123

Exon 2: 124..938

1 ccaaagagga gtatggtttc atggtttgag ttctaatttc aattctgtaa aaaataacta  
 61 ccttggaat gttgtgtctg ctaacacatg ataacgttct catttttctt ttcctttttt  
 121 tagaaacgtt aaaggaaatt gatgatgtct acgaaaaata taagaaagaa gatgatttaa  
 181 accagaagaa acgtctacag cagcttctcc agagagcact aattaatagt caagaattgg  
 241 gagatgaaaa aatacagatt gttacacaaa tgctcgaatt ggtggaaaat cgggcaagac  
 301 aaatggagtt acactcacag tgtttccaag atcctgctga aagtgaacga gcctcagata  
 361 aagcaaagat ggattccagc caaccagaaa gatcttcaag aagaccccg caggcagcgg  
 421 ccagtgaag ccgtgattta tgtcacatgg caaatgggat tgaagactgt gatgatcagc  
 481 cacctaaaga aaagaaatcc aagtcagcaa agaaaaagaa acgctccaag gccaaagcagg  
 541 aaaggggaagc ttcacctgtt gagtttgcaa tagatcctaa tgaacctaca tactgcttat  
 601 gcaaccaagt gtcttatggg gagatgatag gatgtgacaa tgaacagtgt ccaattgaat  
 661 ggtttcaactt ttcatgtgtt tcacttacct ataaaccaa ggggaaatgg tattgcccaa  
 721 agtgcagggg agataatgag aaaacaatgg acaaaagtac tgaaaagaca aaaaaggata  
 781 gaagatcgag gtagtaaagg ccatccacat tttaaagggt tatttgtctt ttatataatt  
 841 cgtttgcttt cagaaaatgt tttagggtaa atgcataaga ctatgcaata atttttaatc  
 901 attagtatta atggtgtatt aaaagttgtt gtactttgtc tgtgacctta attttctgca  
 961 ctgagttacc aaat